Application of GA package in functional packaging

D A Belousova, E E Noskova, D V Kapulin

Siberian Federal University, 79 Svobodny pr., 660041 Krasnoyarsk, Russia

E-mail: ENoskova@sfu-kras.ru

Abstract. The approach to application program for the task of configuration of the elements of the commutation circuit for design of the radio-electronic equipment on the basis of the genetic algorithm is offered. The efficiency of the used approach for commutation circuits with different characteristics for computer-aided design on radio-electronic manufacturing is shown. The prototype of the computer-aided design subsystem on the basis of a package GA for R with a set of the general functions for optimization of multivariate models is programmed.

1. Introduction

In subdivisions of a radio-electronic manufacturing designer, the process of engineering of the radio-electronic equipment (REE) begins with meeting the challenge of functional packaging of the commutation circuit elements. The functional packaging is a planned distribution of commutation circuit elements to printed circuit boards according to the selected optimality criterion. The problem consists in finding the set of the best solutions among the set of all possible alternatives based on the optimality criterion. The complexity of making decisions about such a diverse set of problems is compounded by creating the general functions of global optimization. Global extremum searching requires a large number of computing resources.

Now during the radio-electronic manufacturing, the task of REA functional packaging is often carried out in a manual mode because of the lack of the appropriate algorithms and optimality criteria in the modern CAD systems. The designer, receiving the circuit diagram, works out functional packaging and placement manually using the developed database of elements.

In reviewing the designer work of the manufacturing enterprise with CAD, it is important to note that redesigning CAD systems considers functionality extension and libraries and design methods upgrade. This is a difficult task for a third-party programmer because of impossibility of access to the source code CAD system.

Targets software is very actual as workstation maintaining software. A concrete example of such tool is a developed application.

2. Materials and methods

The R language was chosen as an advanced statistical computing system with very high quality graphics that is freely available for most computing platforms [1].

A chosen directed search tool is an R package GA, implementing an optimization functional of the multidimensional model using genetic algorithms. A universal set of tools, provided by the package, is useful for directed search in a discrete case. The package is also one of the most popular through its developing flexibility and adapting in all forms of fitness-functions [2].

Input data are presented by the internodal connections graph, its adjacency matrix R and element pool matrix Q. R = $||r_{sl}||_{n\times n}$, where n is an amount of elements in the scheme. Q = $||q_{ij}||_{n\times m}$, where n is an amount of elements in the scheme, m is the amount of circuits [3]. These matrixes are compiled by the netlist file processing. Netlist files are generated by any of modern CAD systems (Cadence; DeltaDesigner, etc) through the circuit layout developing process.
The proposal would present separation of circuit's elements set E into two disjoint sets.

$$\mathrm{T}_s = \{e_{s_1}, \dots e_{s_k}\},\ \mathrm{T}_1 \cap \mathrm{T}_2 = \emptyset,\ \ \cup_{s=1}^{2} \mathrm{T}_s = E.$$

Under those conditions, it is required to do element packaging from set E into assemblies $\mathrm{T}_1$and T_2 with minimal connections between them.

3. Functional packaging in genetic algorithm package GA stages.
The option of a graph partitioning in the algorithm is presented as one-dimensional matrix $\tilde{T}$= $||t_{ij}||_{n\times 1}$, где $t_{ij} \in \{1, 2\}$, where t_{ij} is a number of a set assigned with i-st element from the E set. Each genotype stores only a current version of partitioning, providing a disjoint condition and a wide range of solutions with the amount of different elements in subsets [4].

The fitness function is based on quantitative measures of internodal connectivity:

$$S = \frac{1}{2}\sum_{s=1}^{n}\sum_{l=1}^{n} r_{sl},$$

where $r_{sl}$is determined by:

$$r_{sl} = \sum_{e_i \in T_s}\sum_{e_j \in T_s} r_{ij},$$

where $r_{ij}$is a current R matrix element [3].

Crossover is defined by default functionality of the GA package with crossover probability between genotypes equal to 0,8. Quantity of genotypes, presenting elitism, is also defined by default and its value if there are 5% of the current population quantity.

This method was tested on a sample, contains 100 scheme graphs with vertices number equal up to 100 objects (circuit's elements) with different genetic algorithm parameters and the best results were observed under the following conditions: 250 iterations, 50 objects in population, elitism equal to 5% and crossover probability equal to 0,8.

For uniformity monitoring defined special function, defining ratio of subsets' elements amounts. During experiment ratio was equal to 3:2 for two sets.

The authors have conducted a computational experiment on a personal computer with the Intel (R)Core (TM)i7-7820HQ processor with a frequency 2.90GHz. The following benefits of the GA package were detected in the experiment: while package arguments were changing, the results always remains steady; the algorithm shows the same effectiveness for graphs with different amounts of vertices and edges.

Partition option, provided by genetic algorithm, is shown in Figure 1.

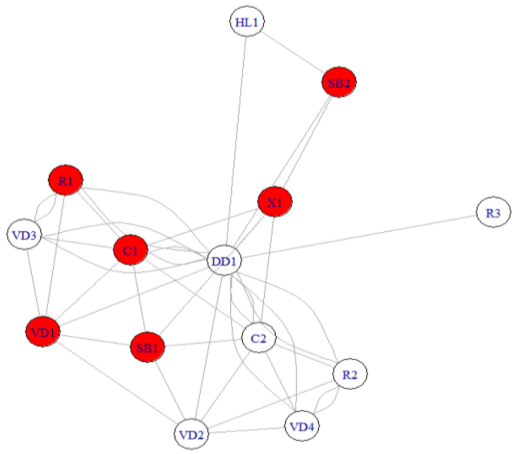


Figure 1 – Partition option for graph with 13 vertices, made by developed algorithm. Partition is made with 250 iterations, 50 objects in population, elitism equal to 5% and crossover probability equal to 0,8. Assignment to subsets is shown by different colors.

4. Results and discussion

The genetic algorithm was tested on a sample; it contains 100 scheme graphs with the vertices number equal up to 100 objects.

For all graphs, the following GA package parameters were defined:

Table 1. GA package parameters in computational experiment with 100 scheme graphs

N	Parameter	Value	Parameter defined
1	Population quantity	50 objects	As argument
2	Number of iterations	250 iterations	As argument
3	Elitism	5%	By default
4	Crossover Probability	0,8	By default

The following is a code, initializing parameters for the main function of genetic algorithm:
ga(fitness = fitness_GA, type = "binary", nBits = ncol(mymatrixQ), popSize = 50, maxiter = 250, monitor = FALSE)

The experiment established that a variety of genotypes about the number of iterations in the functional packaging task are not always translated into partition uniformity, especially for schemes with the number of vertices equal to 100 or more. This is due to the facts that when approaching to the last iterations, especially with higher elitism coefficient, genotypes with a high connectivity or with a low uniformity survive too.

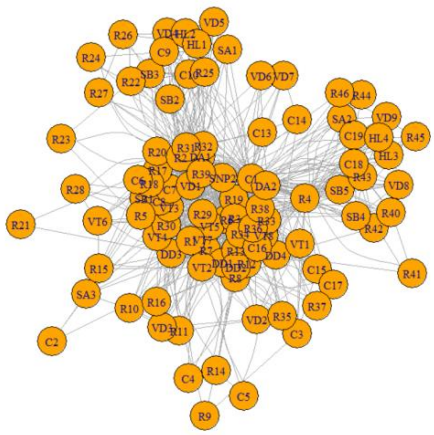
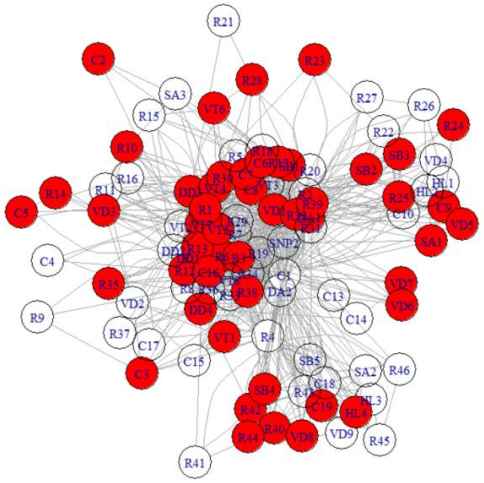
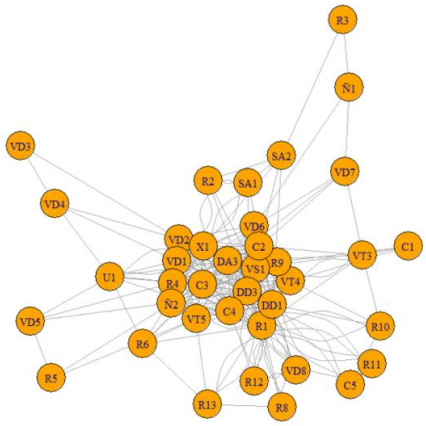
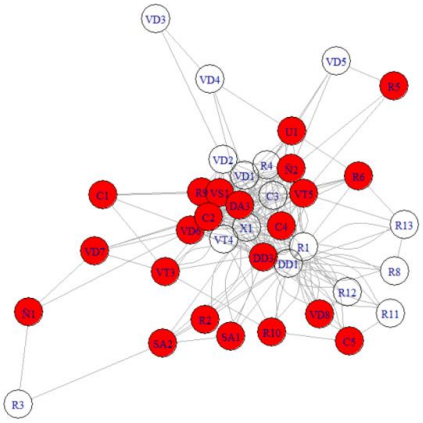
While reducing the number of genotypes in population, lowering the elitism coefficient, defining of crossover function, and a clear increase in the number of iterations of the problem goes away. The ratio of the population number to iteration number was chosen equal to 1:5 empirically.

Below there is table 2, which contains numerical results of the experiment, and table 3, which contains output graphic representation. Assignment to subsets is shown by different colors.

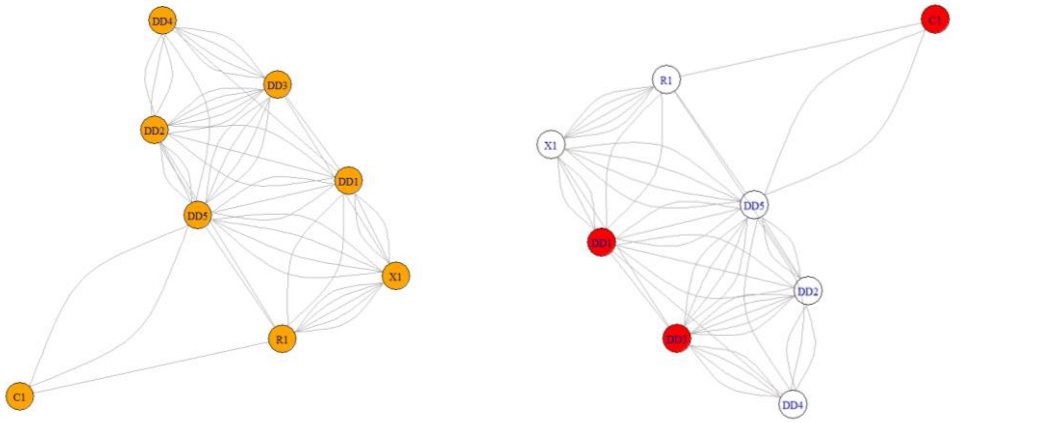
Table 2. Numerical results of the experiment with 100 scheme graphs

	Vertex number	Edges number	CPU performance	Connectivity amount between subsets	Vertex number in T1 set	Vertex number in T2 set
Scheme 1	99	1052	417.28 sec	462	50	49
Scheme 2	38	254	127.91 sec	103	17	21
Scheme 3	8	48	16.74 sec	19	3	5

Table 3. Output graphic representation of the experiment with 100 scheme graphs

	Original graph	Partition option, provided by genetic algorithm
Scheme 1		
Scheme 2		

Scheme 3



5. Conclusion

Through the research efficient and effective prototype, a product was developed, providing an opportunity to create a partitioning option for different sized circuits at reasonable time.

An accessibility of introducing the developed software solution in enterprises of the region is provided by using the free development environment. Speed and effectiveness of results are achieved through a directed search with a genetic algorithm.

The developed algorithm can be used in CAD enterprise systems without modifications only for circuits with the number of elements equal to 100 or less (presented by the real experiment). Time requires that computations can be easily predicted based on scheme characteristics. For circuits with the number of elements equal to 100 or more, the increase of population parameters and the number of iterations is required. It is possible to control it automatically because of algorithm flexibility [1].

In the future, the authors intend to research the possibilities of directed search algorithm combination in order to find better solutions based on the development environment. Also further on, it is planned to research comparing possibilities of different genetic and evolutionary methods for solving CAD design problems.

6. Acknowledgments

This work was supported by the Ministry of Education and Science of the Russian Federation in the framework of the Federal target program «Research and development of priority directions of development of the scientific-technological complex of Russia for 2014-2020» (agreement № 14.575.21.0142, unique ID project RFMEFI57517X0142).

References

[1] Ripley B D 2001 *The R Project in Statistical Computing* (Sanford Weisberg, University of Minnesota)

[2] Scrucca L 2016 Package ‘GA’. URL: https://cran.r-project.org/web/packages/GA/GA.pdf (visited on 2/14/2018)

[3] Selutin V A 1977 *Computer-aided design of electronic devices* (Moscow: Soviet radio)

[4] Muromtsev D U, Turin D V 2014 *CAD software support* (St. Petersburg; Moscow; Krasnodar: Lan)